

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 12:30:08 ; Search time 28 Seconds
(without alignments)
2.963 Million cell updates/sec

Title: SHORT-PEP
Perfect score: 16
Sequence: 1 rw 2

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of matches is 38 (with chosen parameters): 38

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	5	1	UF01_MOUSE
2	13	81.2	5	1	BPP7_BOTIN
3	11	68.8	4	1	OCF3_OCTMT
4	7	43.8	5	1	FARP_AATTR
5	7	43.8	5	1	PRCT_PERAM
6	6	37.5	4	1	FAR3_HIRME
7	6	37.5	4	1	FAR4_HIRME
8	6	37.5	4	1	FLRF_HIRME
9	6	37.5	4	1	FLRF_MACNT
10	5	31.2	4	1	FLRN_ANTEL
11	5	31.2	4	1	FYRI_ANTEL
12	5	31.2	4	1	TUFT_HUMAN
13	2	12.5	3	1	GRMN_HUMAN
14	2	12.5	3	1	LUXE_VIBFT
15	2	12.5	4	1	DCMS_PSECH
16	2	12.5	4	1	FFKA_CARMA
17	2	12.5	5	1	AL14_CARMA
18	2	12.5	5	1	PSK_DAUCA
19	2	12.5	5	1	TRM3_ECOLI
20	1	6.2	3	1	THYL_PIG
21	1	6.2	4	1	ACHL_ACHFU
22	1	6.2	4	1	OCPL_OCTMT
23	1	6.2	5	1	EIO3_LITRU
24	1	6.2	5	1	EIO4_LITRU
25	1	6.2	5	1	PAV2_PARMA
26	1	6.2	5	1	RE11_LITRU
27	1	6.2	5	1	RE21_LITRU
28	1	6.2	5	1	RE31_LITRU
29	1	6.2	5	1	RE32_LITRU
30	1	6.2	5	1	SUGA_ACHDO
31	1	6.2	5	1	TPIS_CANFA
32	1	6.2	5	1	UC22_YAIZE
33	0	0.0	4	1	DCML_PSECH

34	0	0.0	4	1	EOS1_HUMAN
35	0	0.0	4	1	RM01_YEAST
36	0	0.0	5	1	BIOA_CITFR
37	0	0.0	5	1	BIOB_CITFR
38	0	0.0	5	1	UXA4_CHLFR
					P02731 homo sapien
					P36515 saccharomyc
					P13071 citrobacter
					P12997 citrobacter
					P38005 chlamydia t

ALIGNMENTS

RESULT 1
ID UF01_MOUSE STANDARD: PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 KDa.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.le+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 4 RW 5
RESULT 2
ID BPP7_BOTIN STANDARD: PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
enzyme inhibitor).
OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR; G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1 1
PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 5 AA; 629 MW; 776DC37326B0000 CRC64;

Query Match 81.2%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RW 2
1
DB 2 KW 3

RESULT 3

OCP3_OCTMI STANDARD; PRT; 4 AA.
AC P58649;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Cephalopoda; Coleoidea; Octopoda;
OC Incurtata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]

RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.

RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;

RA Iwakoshi E., Hisada M., Minakata H.;

RT "Cardioactive peptides isolated from the brain of a Japanese octopus,

RT Octopus minor.";

RL Peptides 21:623-630(2000).

CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
inotropic effects on the heart. Ocp-4 is a 1000 time less

CC active than Ocp-3.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: Ocp-4 has D-Ser instead of L-Ser.

CC -1- MASS SPECTROMETRY: MM=395.2; METHOD=MALDI.

KW Hormone; D-amino acid.

FT MOD_RES 2 D-SERINE (IN OCP-4).

SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 68.8%; Score 11; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 W 2
1
DB 3 W 3

RESULT 4

FARP_ARTTR STANDARD; PRT; 5 AA.
AC P41853;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE FMRamide-like neuropeptide RYIRF-amide.

OS Arthropoda; Insecta; Diptera; RYIRF-amide.

OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Sericata; Tricladida;

OC Terricola; Geoplinidae; Arthropodidae;

OX NCBI_TaxID=132421;

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RX MEDLINE=94211927; PubMed=7909164;

RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;

RT "RYIRFamide: a turbellarian FMRamide-related peptide (FARP).";

RL Regul. Pept. 50:37-43(1994).

-1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)

CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 5 AMIDATION.

SQ SEQUENCE 5 AA; 754 MW; 69D4004B44600000 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 5;

Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RW 2
1
DB 1 RY 2

RESULT 5

PRCT_PERAM STANDARD; PRT; 5 AA.
AC P01373;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE Proctolin

OS Periplaneta americana (American cockroach),

OS Limulus polyphemus (Atlantic horseshoe crab), and

OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;

OC Blattodea; Blattidae; Periplaneta.

OX NCBI_TaxID=6978, 6850, 6759;

RN [1]

RP SEQUENCE.

RC SPECIES=P. americana;

RX MEDLINE=76074708; PubMed=576;

RA Starratt A.N., Brown B.E.;

RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter

in insects.";

RL Life Sci. 17:1253-1256(1975).

RN [2]

RP BIOLOGICAL SOURCE.

RC SPECIES=P. americana;

RX MEDLINE=81225865; PubMed=6113690;

RA O'Shea M., Adams M.E.;

RT "Pentapeptide (proctolin) associated with an identified neuron.";

RL Science 213:567-569(1981).

RN [3]

RP SEQUENCE.

RC SPECIES=L. polyphemus;

RX MEDLINE=90287800; PubMed=2356151;

RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.;

RA Watson W.H., III, Hunt D.F., Griffin P.R., Alexander J.E.;

RA Shabanowitz J.;

RT "Identification of proctolin in the central nervous system of the

horseshoe crab, Limulus polyphemus.";

RL Peptides 11:205-211(1990).

RN [4]

RP SEQUENCE.

RC SPECIES=C. maenas;

RX MEDLINE=86232789; PubMed=2872661.

RA Stangier J., Dirksen H., Keller R.;

RT "Identification and immunocytochemical localization of proctolin in

pericardial organs of the shore crab, Carcinus maenas.";

RL Peptides 7:67-72(1986).

CC -1- FUNCTION: STIMULATES CARDIAC PUMP AND HINDGUT MOTILITY,

MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.

CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN

THE CRAB PERICARDIAL ORGANS.

CC PIR: A01644; HOROHA.

DR PIR: A60411; A60411.

KW Neuropeptide.

SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 5;

Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RW 2
1

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DB      1 RW 2
RESULT 6
FAR4_HIRME      STANDARD;      PRT;      4 AA.
AC      P42562;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DE      FLRFamide.
DE      FMRFamide-like neuropeptide YMRF-amide.
OS      Hirudo medicinalis (Medicinal leech).
OC      Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OX      NCB1_TaxID=6421;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=92195954; PubMed=1686933;
RA      Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT      "Identification of Rfamde neuropeptides in the medicinal leech.";
RL      Peptides 12:897-908(1991).
CC      -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC      FAMILY.
KM      Neuropeptide; Amidation.
FT      MOD.RES      4 AA; 598 MW; 69D4073830000000 CRC64;
SQ      SEQUENCE      4 AA; 598 MW; 69D4073830000000 CRC64;

Query Match      37.5%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RW 2
DB      1 RW 2
DE      3 RF 4
RESULT 7
FAR4_HIRME      STANDARD;      PRT;      4 AA.
AC      P42563;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DE      FMRFamide-like neuropeptide YMRF-amide.
OS      Hirudo medicinalis (Medicinal leech).
OC      Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OX      NCB1_TaxID=6421;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=92195954; PubMed=1686933;
RA      Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT      "Identification of Rfamde neuropeptides in the medicinal leech.";
RL      Peptides 12:897-908(1991).
CC      -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC      FAMILY.
KM      Neuropeptide; Amidation.
FT      MOD.RES      4 AA; 616 MW; 69D4068B30000000 CRC64;
SQ      SEQUENCE      4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match      37.5%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RW 2
DB      1 RW 2
DE      3 RF 4
RESULT 8
FLRF_HIRME      STANDARD;      PRT;      4 AA.
AC      P42561;

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DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DE      FLRFamide.
DE      FMRFamide.
OS      Hirudo medicinalis (Medicinal leech), and
OS      Helisoma trivolvis (Snail).
OC      Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OX      NCB1_TaxID=6421, 27815;
RN      [1]
RP      SEQUENCE.
RX      SPECIES-H.medicalis;
RX      MEDLINE=92195954; PubMed=1686933;
RA      Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT      "Identification of Rfamde neuropeptides in the medicinal leech.";
RL      Peptides 12:897-908(1991).
RN      [2]
RP      SEQUENCE.
RX      SPECIES-H.trivolvis; TISSUE=Kidney;
RX      MEDLINE=94286417; PubMed=7912428;
RA      Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT      "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT      trivolvis".
RL      Peptides 15:31-36(1994).
CC      -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC      FAMILY.
KM      Neuropeptide; Amidation.
FT      MOD.RES      4 AA; 582 MW; 69D40729A0000000 CRC64;
SQ      SEQUENCE      4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match      37.5%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RW 2
DB      1 RW 2
DE      3 RF 4
RESULT 9
FMRF_MACNT      STANDARD;      PRT;      4 AA.
AC      P01162;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DE      15-JUL-1998 (Rel. 36, Last annotation update)
DE      FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS      Macrocallista nimbosa (Sun-ray clam),
OS      Nerereis virens (Sandworm),
OS      Hirudo medicinalis (Medicinal leech), and
OS      Helisoma trivolvis (Snail).
OC      Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OX      NCB1_TaxID=6594, 6353, 6421, 27815;
RN      [1]
RP      SEQUENCE, AND SYNTHESIS.
RX      SPECIES-M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;
RX      MEDLINE=77215956; PubMed=877582;
RA      Price D.A., Greenberg M.J.;
RT      "Structure of a molluscan cardioexcitatory neuropeptide.";
RL      Science 197:670-671(1977).
RN      [2]
RP      SEQUENCE, AND CHARACTERIZATION.
RX      SPECIES-M.nimbosa; TISSUE=Ganglion;
RX      MEDLINE=78012038; PubMed=909875;
RA      Price D.A., Greenberg M.J.;
RT      "Purification and characterization of a cardioexcitatory neuropeptide
RL      Prep. Biochem. 7:261-281(1977).
RN      [3]
RP      SEQUENCE.
RX      SPECIES-N.virens;
RX      MEDLINE=90259866; PubMed=2342992;

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RA Krajinak K.G., Price D.A.;
RT "Authentic FMRFamide is present in the polychaete Nereis virens.";
RN Peptides 11:75-77(1990).
[4]
RP SEQUENCE.
RC SPECIES-H.medicalis; PubMed=1686933;
RA Evans B.D., Pohl J., Katsolis M.A., Calabrese R.L.;
RT "Identification of Rfamde neuropeptides in the medicinal leech.";
RN Peptides 12:897-908(1991).
[5]
RP SEQUENCE.
RC SPECIES-H.trivolvus; TISSUE-Kidney;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
trivolvus.";
RN Peptides 15:31-36(1994).
[1]
CC -1- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
CARDIAC CONTRACTION.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
DR PIR: A01426; ECKM.
DR PIR: A60418; A60418.
RW Neuropeptide: Amidation.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RW 2
1:
Db 3 RF 4

RESULT 10
FLRN_AMEL STANDARD; PRT; 4 AA.
AC P58707;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antho-Rfamde.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
CC Nyantheae; Actiniidae; Anthopleura.
NX NCBI_TaxID=6110;
[1]
RP SEQUENCE, AND MASS-SPECTROMETRY.
RA MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheld R.K., Notchaker H.-P., Staley A.L.;
RT "Isolation of L-3-phenylactyl-Leu-Arg-Asn-NH2 (Antho-Rfamde), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
RN Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron-specific.
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NX NCBI_TaxID=9606;
[1]
RW MOD_RES 1 1 L-3-PHENYLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 31.2%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 R 1
1:

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Db 3 R 3

RESULT 11
FLRN_AMEL STANDARD; PRT; 4 AA.
AC P58706;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antho-Rfamde I [contains Antho-Rfamde II].
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
CC Nyantheae; Actiniidae; Anthopleura.
NX NCBI_TaxID=6110;
[1]
RP SEQUENCE.
RA MEDLINE=92270459; PubMed=1821096;
RA Notchaker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
biologically active L-3-phenylactyl-Tyr-Arg-Ile-NH2 and its
des-phenylactyl fragment Tyr-Arg-Ile-NH2.";
RN Peptides 12:1165-1173(1991).
[2]
RW MOD_RES 1 1 ANTHO-RIAMIDE I.
FT MOD_RES 2 4 ANTHO-RIAMIDE II.
FT MOD_RES 1 1 L-3-PHENYLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 31.2%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 R 1
1:
Db 3 R 3

RESULT 12
FLRN_AMEL STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NX NCBI_TaxID=9606;
[1]
RW MOD_RES 1 1
FT MOD_RES 4 4
SQ SEQUENCE.
RA MEDLINE=72187087; PubMed=4112769;
RA Nishio K., Constantinopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin.";
RN Biochem. Biophys. Res. Commun. 47:172-179(1972).
[2]

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RP IMMUNOGLOBULIN CLASS.
 RX MEDLINE=68091045; PubMed=4169272;
 RA Fidalgo B.V., Najjar V.A.;
 RT "The physiological role of the lymphoid system. VI. The stimulatory
 effect of leucophilic gamma globulin (leucocinin) on the phagocytic
 activity of human polymorphonuclear leucocyte."
 RT Biochemistry 6:336-339(1967).
 CC -1- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
 CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
 MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
 CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
 ACTIVITY OF NEUTROPHILS.
 DR PIR: A02147; A02147.
 DR MIM: 191150; .
 SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;
 Query Match 31.2%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 R 1
 DB 4 R 4

RESULT 13
 GRM_HUMAN STANDARD; PRT; 3 AA.
 ID GRM_HUMAN
 AC P01157;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Growth-modulating peptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=77162369; PubMed=858356;
 RA Schlesinger D.H., Pickart L., Thaler M.M.;
 RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine."
 RL Experientia 33:324-325(1977).
 CC -1- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
 GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
 DR PIR: A01421; GKHU.
 SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;
 Query Match 12.5%; Score 2; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 1.1e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 R 1
 DB 3 K 3

RESULT 14
 LUXE_VIBFI STANDARD; PRT; 3 AA.
 ID LUXE_VIBFI
 AC P24272;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
 protein synthetase) (Fragment).
 LOXE.
 GN Vibrio fischeri.
 OS Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.
 OC NCBI_TaxID=668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91072226; PubMed=2254256;

RA Swartzman E., Kapoor S., Graham A.F., Maignen E.A.;
 RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
 site for the lux operon."
 RT J. Bacteriol. 172:6797-6802(1990).
 CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
 IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
 FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
 SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
 CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
 an acyl-protein thioester.
 CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
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 DR EMBL: M62812; -; NOT_ANNOTATED_CDS.
 DR LUMINESCENCE; Ligase.
 FT NON_TER 1
 SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;
 Query Match 12.5%; Score 2; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 1.1e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 R 1
 DB 2 K 2

RESULT 15
 DCMS_PSECH STANDARD; PRT; 4 AA.
 ID DCMS_PSECH
 AC P19918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
 dehydrogenase subunit S) (CO-DH S) (Fragment).
 GN CUS.
 GN Pseudomonas carboxydhydrogena.
 OS Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group.
 OX NCBI_TaxID=290;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 carboxydotrophic bacteria."
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 acceptor.
 CC -1- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 SMALL.
 DR PIR: P10146; P10146.
 KW Oxidoreductase; Iron-sulfur.
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;
 Query Match 12.5%; Score 2; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1.1e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 R 1

Db 3 K 3

RESULT 16
FFKA_AMEL
ID FFKA_AMEL STANDARD; PRT: 4 AA.

DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antho-Kamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nymphaeae; Actinellidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA "Nothacker H.-P., Rinehart K.L.Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenylactyl-Phe-Lys-Ala-NH2 (Antho-Kamide), a
RT novel neuropeptide from sea anemones."
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kamide and Antho-Riamide."
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron-specific.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 12.5%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 R 1
Db 3 K 3

RESULT 17
AL14_CARMA
ID AL14_CARMA STANDARD; PRT: 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX MEDLINE=98121193; PubMed=9461295;
RA Duvre H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT Allostatin superfamily in the shore crab Carcinus maenas";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.

FT MOD_RES 5 5 AMIDATION (POTENTIAL).
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 12.5%; Score 2; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 W 2
Db 1 Y 1

RESULT 18
PSK_DAUCA
ID PSK_DAUCA STANDARD; PRT: 5 AA.
AC P58261;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phytosulfolokine-alpha (PSK-alpha) [Contains: Phytosulfolokine-beta (PSK-beta)].
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RX STRAIN=cv. US-Hartwickgoun;
RX MEDLINE=20212743; PubMed=10750705;
RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
RA Kanada H., Sakagami Y.;
RT "A secreted peptide growth factor, phytosulfolokine, acting as a
RT stimulatory factor of carrot somatic embryo formation."
RL Plant Cell Physiol. 41:327-32(2000).
CC -1- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
CC EMBRYOS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PHYTOSULFOLOKINE FAMILY.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4 PHYTOSULFOLOKINE-BETA.
FT MOD_RES 1 1 SULFATION.
FT MOD_RES 3 3 SULFATION.
SQ SEQUENCE 5 AA; 687 MW; 76C1BB504B300000 CRC64;

Query Match 12.5%; Score 2; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 W 2
Db 1 Y 1

RESULT 19
TRM3_ECOLI
ID TRM3_ECOLI STANDARD; PRT: 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Trm protein (Fragment).
GN TRM.
OS Escherichia coli.
OS Plasmid IncFII R100.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=68227859; PubMed=2836369;
RA Inamoto S., Yoshioaka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the trax
RT and trax genes of plasmid R100."
RL J. Bacteriol. 170:2749-2757(1988).
CC
CC -1- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.
CC -----
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CC -----
DR EMBL: M20941; -, NOT_ANNOTATED.CDS.
DR PIR: A32014; A32014.
KM Conjugation: plasmid; DNA-binding.
FT NON_TER 1
SQ SEQUENCE 5 AA: 634 MW: 68181AA43500000 CRC64;

Query Match 12.5%; Score 2; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
Db 1 K 1

RESULT 20
THYL_PIG STANDARD: PRT; 3 AA.
ID THYL_PIG
AC P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thylolberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
OS Sus scrofa (Pig),
OS Ovis aries (Sheep),
OS Bombina orientalis (Oriental fire-bellied toad), and
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823; 9940; 8346; 8316;
RN [1]
RP SEQUENCE.
RC SPECIES-Pig; TISSUE-Hypothalamus;
RX MEDLINE=70136150; PubMed=4984938;
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
RT "Structure of porcine thyrotropin releasing hormone."
RL Biochemistry 9:1103-1106(1970).
RN [2]
RP SYNTHESIS.
RC SPECIES-Pig;
RX MEDLINE=70039904; PubMed=4982117;
RA Bolter J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
RT "The identity of chemical and hormonal properties of the thyrotropin
RT releasing hormone and pyroglutamyl-histidyl-proline amide."
RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
RN [3]
RP SEQUENCE.
RC SPECIES-Sheep; TISSUE-Hypothalamus;
RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,
RA Ward D.N.;
RT "The elucidation of the primary structure of the hypothalamic thyroid
RT stimulating hormone releasing factor of ovine origin by means of mass
RT spectrometry."
RL Org. Mass Spectrom. 5:221-228(1971).
RN [4]

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RP SYNTHESIS.
RC SPECIES-Sheep;
RX MEDLINE=70163386; PubMed=4985794;
RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
RA Guillemin R.;
RT "Characterization of ovine hypothalamic hypophysiotropic
RT TSH-releasing factor."
RL Nature 226:321-325(1970).
RN [5]
RP SEQUENCE.
RC SPECIES-B.orientalis; TISSUE-Skin;
RX MEDLINE=7618339; PubMed=815011;
RA Yasuhara T., Nakajima T.;
RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin."
RL Chem. Pharm. Bull. 23:3301-3303(1975).
RN [6]
RP SEQUENCE.
RC SPECIES-N.viridescens;
RX MEDLINE=75035605; PubMed=4214528;
RA Grimm-Joergensen Y., McKelvy J.F.;
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
RT viridescens) brain in vitro. Isolation and characterization of
RT thyrotropin releasing factor."
RL J. Neurochem. 23:471-478(1974).
CC -1- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
DR PIR: A01415; RHPGT.
DR PIR: A93750; RHSHT.
DR PIR: A90919; RHTDT.
DR PIR: A92971; A92971.
KW Amidation.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 3 3 AMIDATION.
SQ SEQUENCE 3 AA: 380 MW: 7761F6B000000000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 3;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
Db 1 Q 1

RESULT 21
ACHIL_ACHFU STANDARD: PRT; 4 AA.
ID ACHIL_ACHFU
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Achatin-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN-Ferussac; TISSUE-Ganglion;
RX MEDLINE=89273551; PubMed=2597281;
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Ll P.,
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT fulica ferussac containing a D-amino acid residue."
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RP CHARACTERIZATION.
RC STRAIN-Ferussac; TISSUE-Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;

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RT "Purification of achatin-I from the atria of the African giant snail,
RT Achatina fulica, and its possible function."
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE-93014529; PubMed-1399265;
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA Ishida T., Nomoto K.;
RT "Crystal structure and molecular conformation of achatin-I
RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
RT D-amino acid residue."
RL Int. J. Pept. Protein Res. 39:258-264(1992).
CC -1- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
DR PIR: A32480; A32480.
KW Hormone; D-amino acid.
FT MOD_RES 2
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 W 2
DB 2 F 2

RESULT 22
OCP1_OCTM1 STANDARD; PRT; 4 AA.
AC P58648;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cardioactive peptides OCP-1/Ocp-2.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incintrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE-Brain;
RX MEDLINE-20336815; PubMed-10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor."
RL Peptides 21:623-630(2000).
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less
CC active than Ocp-1.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: OCP-2 has L-Phe instead of D-Phe.
CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 W 2
DB 2 F 2

RESULT 23
E103_LITRU STANDARD; PRT; 5 AA.
AC P82099;

DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE-Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: SECRETED.
KW Amphibian skin; Amidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 W 2
DB 1 F 1

RESULT 24
E104_LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE-Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: SECRETED.
KW Amphibian skin; Amidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 W 2
DB 1 F 1

RESULT 25
PAP2_PAPMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pardaxin II (PxiI) (Fragment).
OS Pardachirus marmoratus (Red sea mooses sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE-Skin secretion;
RX MEDLINE=87057369; Pubmed=3782138;
RA Lazarovici P., Primor N., Ioew L.M.;
RT 'Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mooses sole (Pardachirus
RT marmoratus).';
RL J. Biol. Chem. 261:16704-16713(1986).
CC -1- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
CC IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC -1- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KM Toxin.
FT NON_TER
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 W 2
DB 2 F 2

RESULT 26
RE21_LITRU
ID RE21_LITRU STANDARD; PRT; 5 AA.
AC P82070;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT 'The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.';
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=538; METHOD=FAB.
KM Amphibian skin.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 W 2
DB 3 F 3

QY 2 W 2
DB 3 F 3

RESULT 27
RE21_LITRU
ID RE21_LITRU STANDARD; PRT; 5 AA.
AC P82071;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT 'The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.';
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KM Amphibian skin.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 W 2
DB 3 F 3

RESULT 28
RE21_LITRU
ID RE21_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT 'The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.';
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KM Amphibian skin; Anidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 W 2
DB 3 F 3

QY 2 W 2
DB 3 F 3

Db 3 F 3

RESULT 29

RE32_LITRU STANDARD: PRT: 5 AA.

AC P82073;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 3.2.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_Taxid=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 Litoria electrica. Comparison with the skin peptides from Litoria
 rubella".
 RT Aust. J. Chem. 52:639-645(1999).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 KW Amphibian skin.
 SQ SEQUENCE 5 AA: 570 MW; 71A9C9C862A00000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 5;

Best Local Similarity 0.0%; Pred. No. 1.1e+05; Indels 0; Gaps 0;

Oy 2 W 2
 Db 3 F 3

RESULT 30

SUGA_ACHDO STANDARD: PRT: 5 AA.

AC P19991;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Suboesophageal ganglion pentapeptide.
 OS Acheta domesticus (House cricket).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;
 OC Gryllidae; Gryllinae; Acheta.
 OX NCBI_Taxid=6997;
 RN [1]
 RP SEQUENCE.
 RA Wicker C., Wicker C.;
 RT "Isolation and structure of a peptide isolated from the
 suboesophageal ganglion of Acheta domesticus (Orthoptera)."
 RT Comp. Biochem. Physiol. 88C:185-187(1987).
 CC -1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
 CC GANGLIA.
 CC PIR: JS0319; JS0319;
 SQ SEQUENCE 5 AA: 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 5;

Best Local Similarity 0.0%; Pred. No. 1.1e+05; Indels 0; Gaps 0;

Oy 2 W 2
 Db 5 F 5

RESULT 31

TPIS_CANFA STANDARD: PRT: 5 AA.

AC P54714;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
 GN Tpi1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins".
 RT Electrophoresis 18:2795-2802(1997).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glyceralone
 CC phosphate.
 CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
 DR HSC-2DPAGE; P54714; DOG.
 DR InterPro: IPR000652; Triophos_1smrse.
 DR PROSITE: PS00171; TIM; PARTIAL.
 KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
 KW Pentose shunt.
 FT NON_TER 1 1
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA: 550 MW; 64444862C9A00000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 5;

Best Local Similarity 0.0%; Pred. No. 1.1e+05; Indels 0; Gaps 0;

Oy 2 W 2
 Db 1 F 1

RESULT 32

UC22_MAIZE STANDARD: PRT: 5 AA.

AC P80628;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_Taxid=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernellet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program".
 RT Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
 CC Maize-2DPAGE; P80628; COLEOPTILE.
 DR MaizeDB; 123954; -.
 FT NON_TER 1 1
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA: 654 MW; 72CB19C9C0300000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 5;

Best Local Similarity 0.0%; Pred. No. 1.1e+05; Indels 0; Gaps 0;

Oy 2 W 2
 Db 1 F 1

Query Match 6.2%; Score 1; DB 1; Length 5;
 Best Local Similarity 0.0%; Pred. NO. 1.1e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 W 2
 DB 2 F 2

RESULT 33

DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN CUTH.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria."
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced acceptor.
 CC -1- COFACTOR: Molybdenum (molybdopterin).
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL.
 DR PIR: P10140; P10140.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 441 MW; 7761876F00000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. NO. 1.1e+05;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 R 1
 DB 3 H 3

RESULT 34

EOSI_HUMAN STANDARD; PRT; 4 AA.
 AC P02731;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Eosinophilic peptides.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eulheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=76078412; PubMed=1060093;
 RA Goebel E.J., Austen K.F.;
 RT "Purification and synthesis of eosinophilic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of anaphylaxis."
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
 CC -1- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG

CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
 CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
 CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
 CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
 DR PIR: A03190; ETHUL.
 FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
 FT FTID=VAR_005201.
 SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

OY 1 R 1
 DB 4 E 4

Query Match 0.0%; Score 0; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. NO. 1.1e+05;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 35

RM01_YEAST STANDARD; PRT; 4 AA.
 AC P36515;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
 GN MRPL.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=91285106; PubMed=2060626;
 RA Grohmann L., Graack H.-R., Kruff V., Choll T., Goldschmidt-Reisin S., Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."
 RL FEBS Lett. 284:51-56(1991).
 DR PIR: S17255; S17255.
 DR SGD: L0002681; MRPL1.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. NO. 1.1e+05;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 R 1
 DB 1 S 1

RESULT 36

BIOA_CITFR STANDARD; PRT; 5 AA.
 AC P13071;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA amino transferase) (Fragment).
 GN BROA.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=89006280; PubMed=2971595;
 RA Shivan D., Campbell A.;

```

RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate -> S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: Biotin biosynthesis.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR InterPro; IPR000954; Aminotran_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KM Biotin biosynthesis; transferase; Aminotransferase;
KW Pyridoxal phosphate.
FT NON_TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAB1B1A6F00000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 R 1
DB 1 M 1

RESULT 37
BIOS_CITR STANDARD; PRT; 5 AA.
AC P12997;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).
GN BIOS.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
CC -1- PATHWAY: Biotin biosynthesis; last step.
CC -1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC FAMILY.
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CC -----
DR EMBL; M21922; -; NOT_ANNOTATED_CDS.
KM Biotin biosynthesis; iron-sulfur; Transferase.
FT NON_TER 5

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SQ SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 R 1
DB 3 H 3

RESULT 38
UXA4_CHLTR STANDARD; PRT; 5 AA.
ID UXA4_CHLTR
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=613;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christensen G., Birkelund S., Vrethou E., Rattl G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 KDa.
DR Slena-2DPAGE; P38005; -;
FT NON_TER 5
SQ SEQUENCE 5 AA; 474 MW; 75BA865AA800000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 R 1
DB 1 X 1

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Search completed: February 21, 2003, 12:31:32
 Job time : 35 secs